

FIG. 2

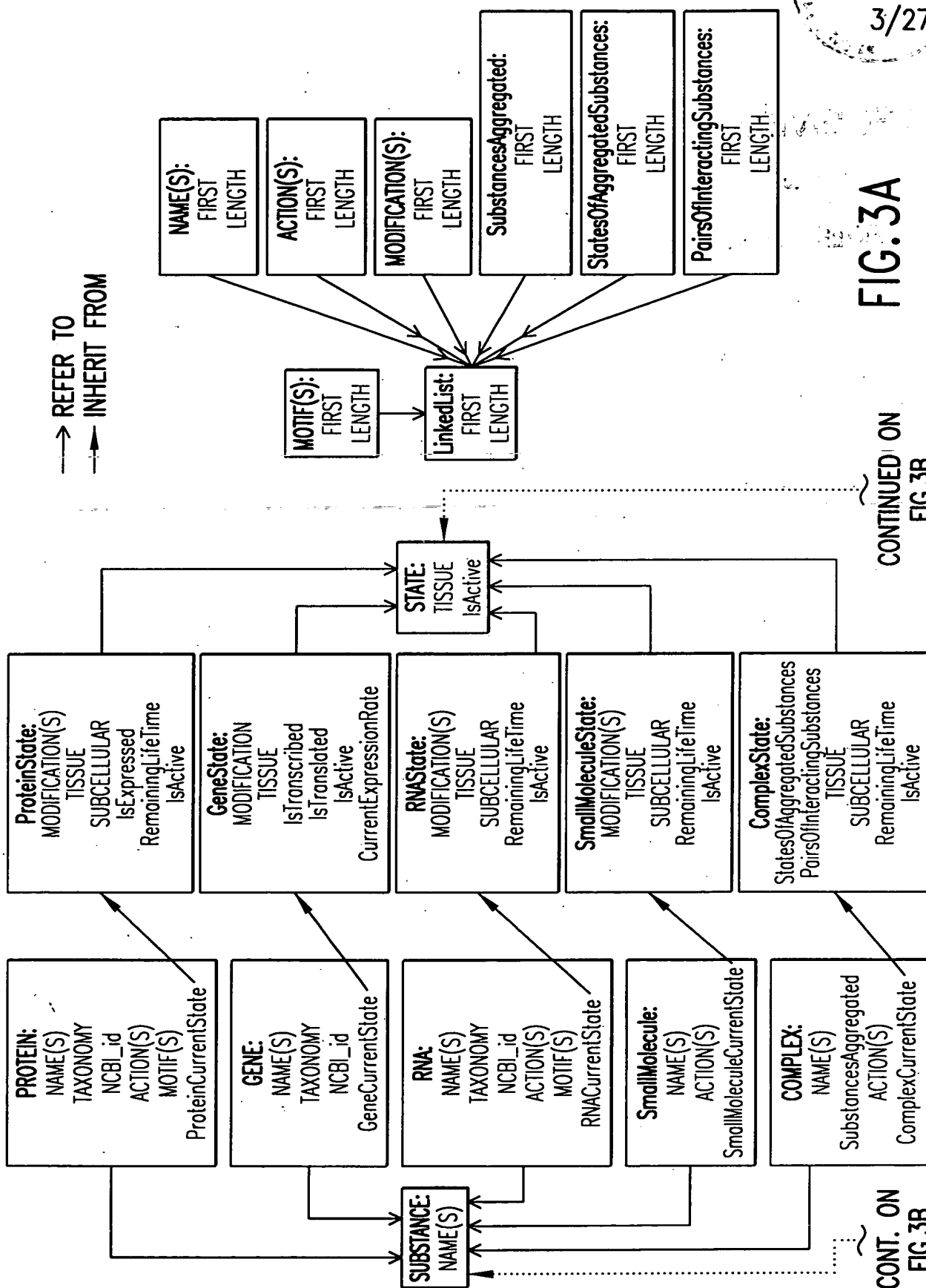
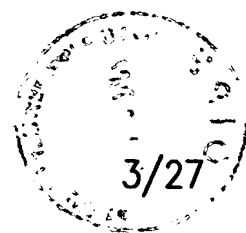


FIG. 3A

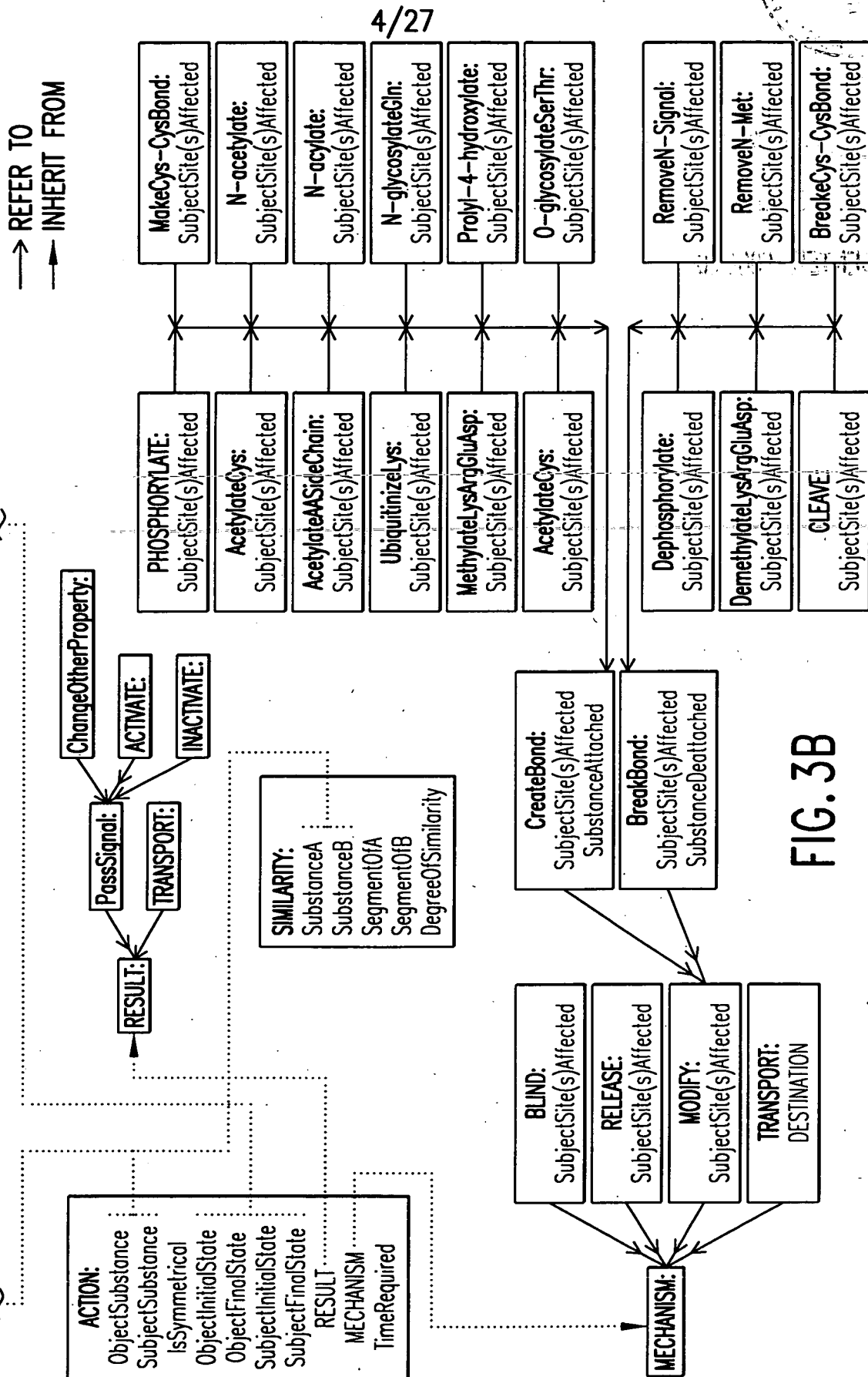
CONTINUED ON  
FIG. 3B

CONT. ON  
FIG. 3B



CONT. FROM  
FIG. 3A

CONTINUED FROM  
FIG. 3A



bci-xL / bci / bci-xS / ced-9 / Bax / Btk / Bak / p21 / NGFI-B / N10 / Nak1 / Nur77 / Nur1 / Nor-1 / Noi-1 / RXR/ galectin-1 / N-glycan  
 / CNTF / lck / fyn / ZAP-70 / raf. / ras / MAP / protein kinase C / PKC / phosphatase calcineurin / NF-AT / AP1 / 14-3-3 / Raf-1 /  
 Bci-2 / interleukin / IL-1 / IL-3 / cytokine / IGF-1 / CD95 / Apo-1 / RIP / FAF1 / FADD / FAP-1 / TNFR / TRAF / TRAP1 /  
 TRAP2 / TRADD / HIAP1 / HIAP2 / CD40 / CD30 / XIAP / CD2 / CD3 / TCR / Bci-w / Mci-1 / NR-13 / BHRF1 / HMM5-HL /  
 E1B19K / Nbk / Mch2 / CPP32 / ICE / FLICE / Nedd-2 / TX / Mch3 / Mch4 / ICB-1s / nor-1 / DNaseI / caspase / MACH1 /  
 Mch5 / apopain / Yama / ICH / CMH / ced-3 / ced-4 / ced-9 / p53 / MKK3 / MKK1 / MKK2 / MKK4 / BAG-1 / Src / FAST/  
 p38 / p42 / ERK1 / p44 / ERK2 / SAPK / JNK / MEK / C-JUN / MEF2D / ATF2 / calcineurin / ELK-1 / protein phosphatase 2A /  
 raf-1 / IL-I beta / TNF / PTK / Apaf / p35 / ETS / C-Myc / IL-2 / IL-2 receptor / NF-kappa B / TNFR-1 / TRAIL / APO-2L /  
 DR4 / death receptor / DR3 / DR2 / DR5 / DR1 / bod / BMPR / BMP-x / TGF / grim / bid / FAN / perforin / Fas-L / Fas / DcR1  
 / decoy receptor / wxi-1 / NGF receptor / growth factor / RAR

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FIG.4



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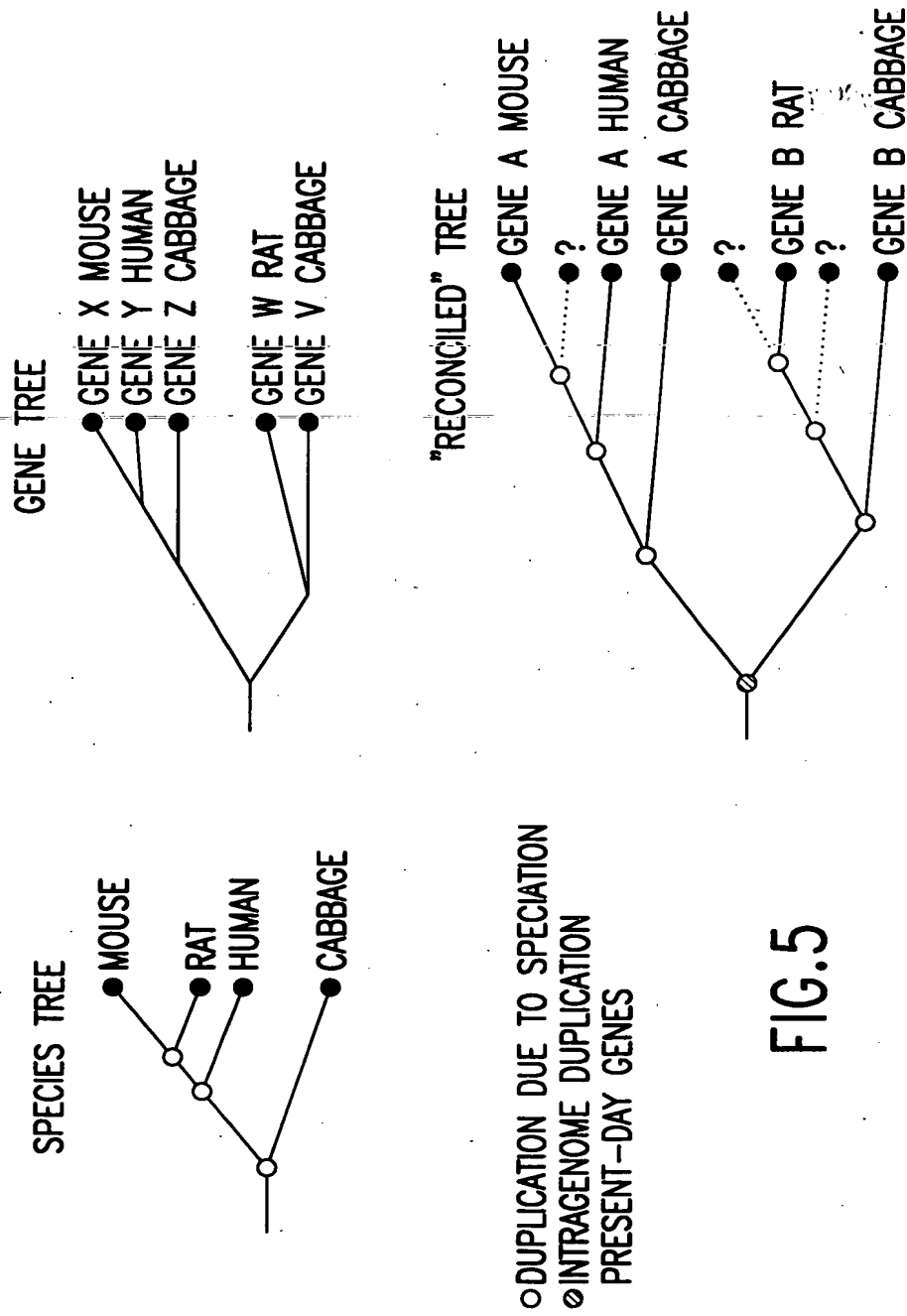
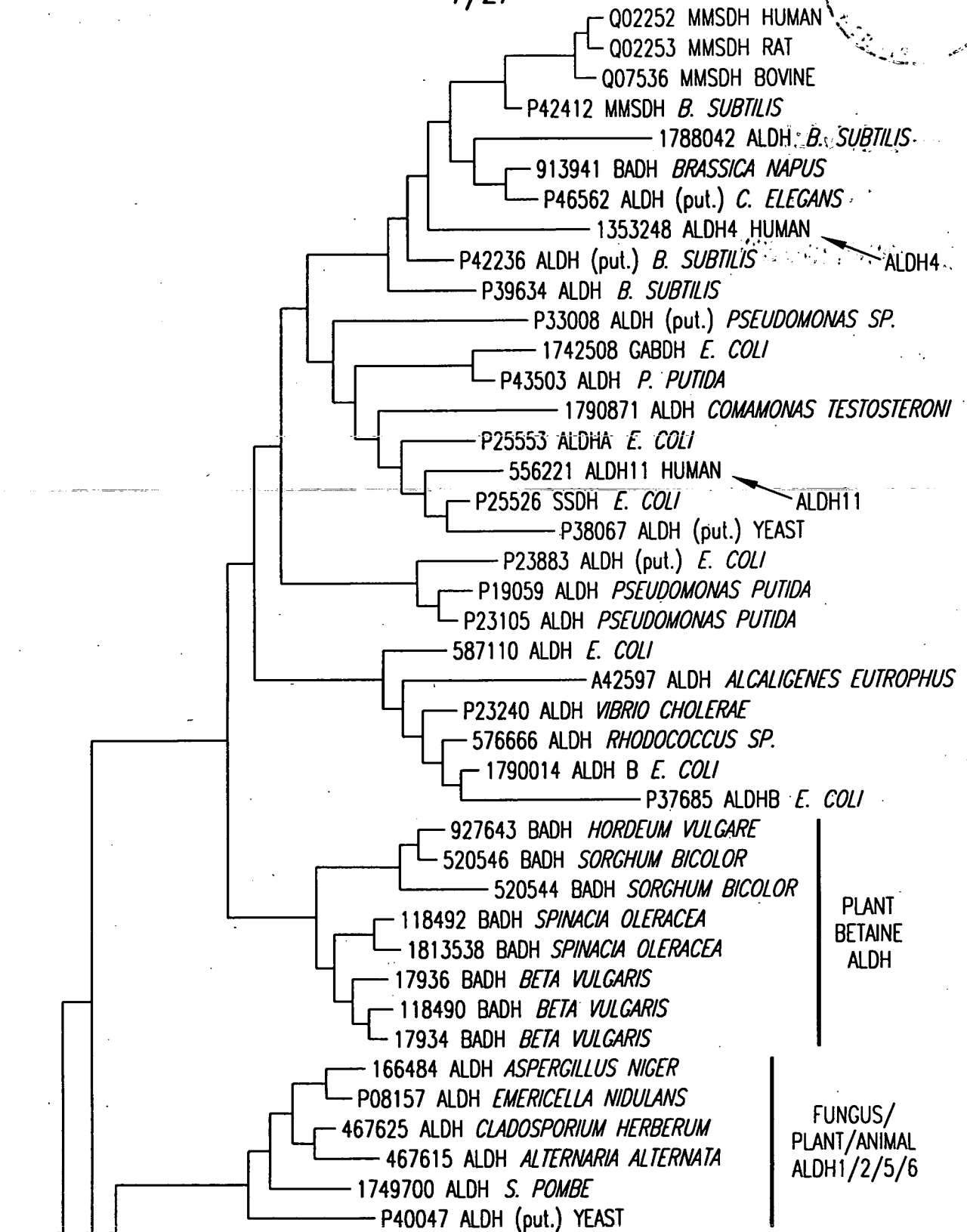
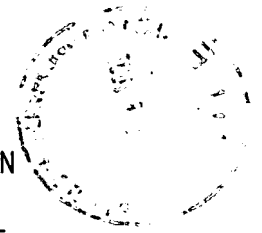


FIG.5

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CONTINUED ON  
FIG.6B

FIG.6A

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CONTINUED FROM  
FIG.6A

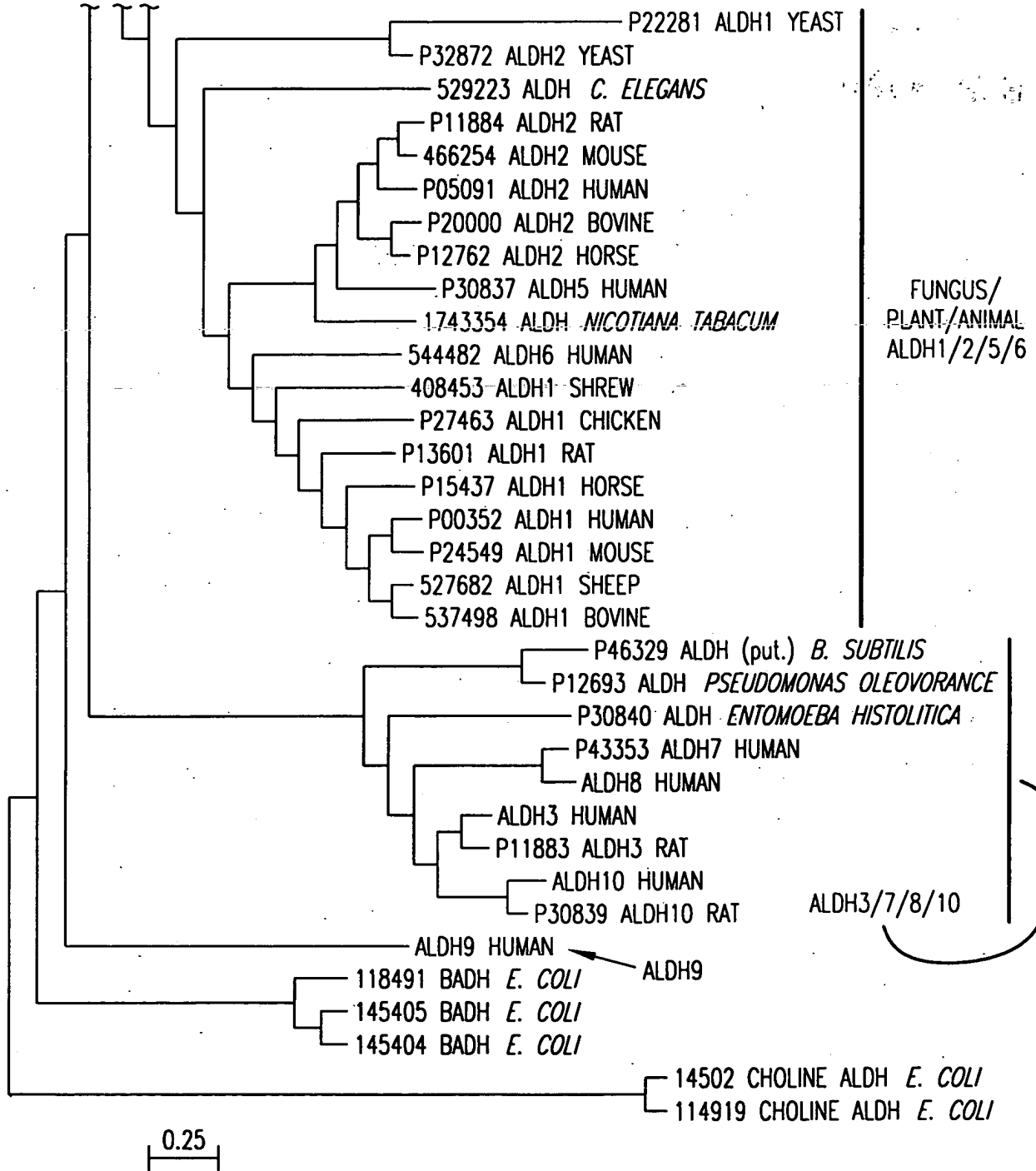


FIG.6B



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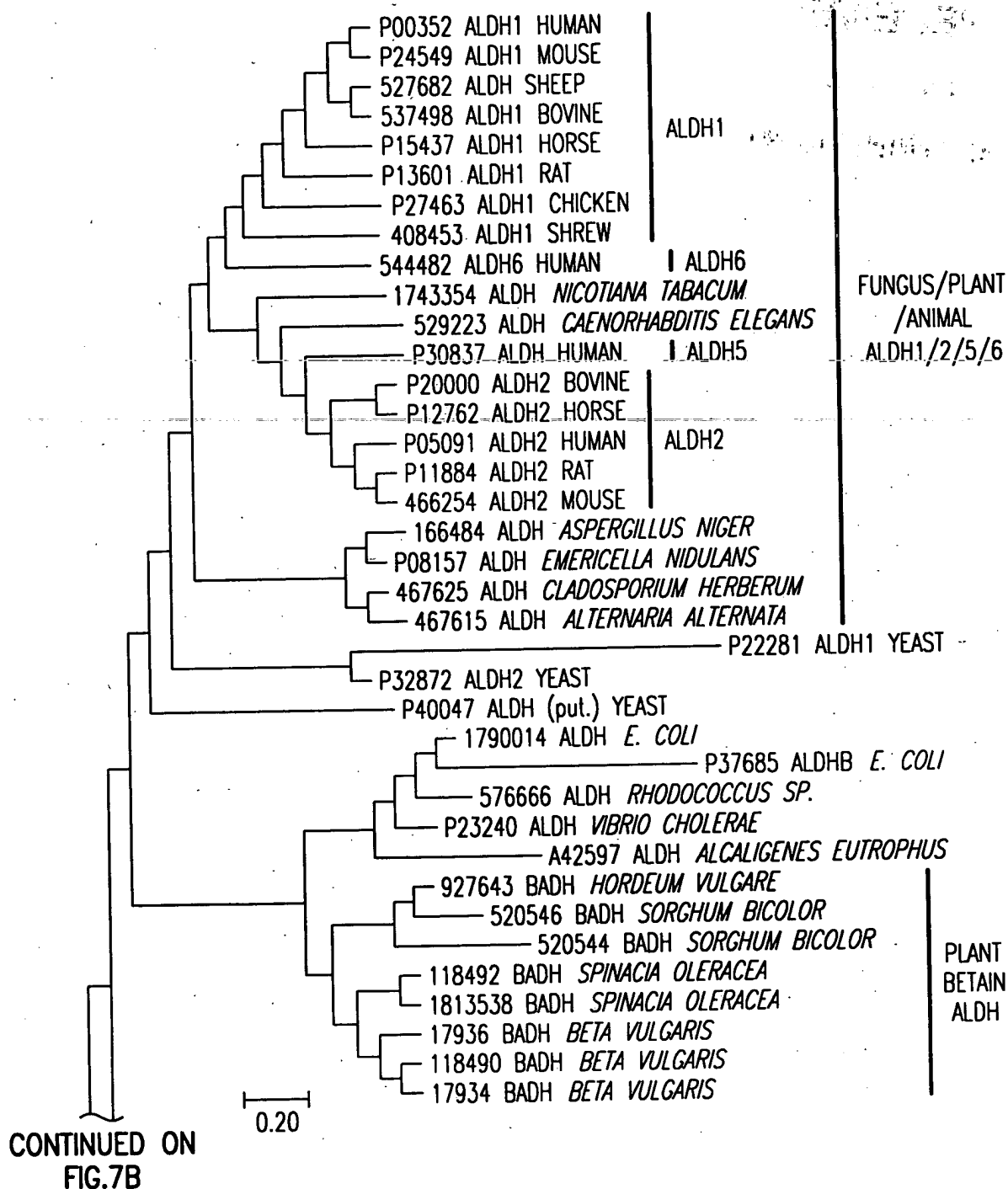


FIG. 7A

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CONTINUED FROM  
FIG.7A

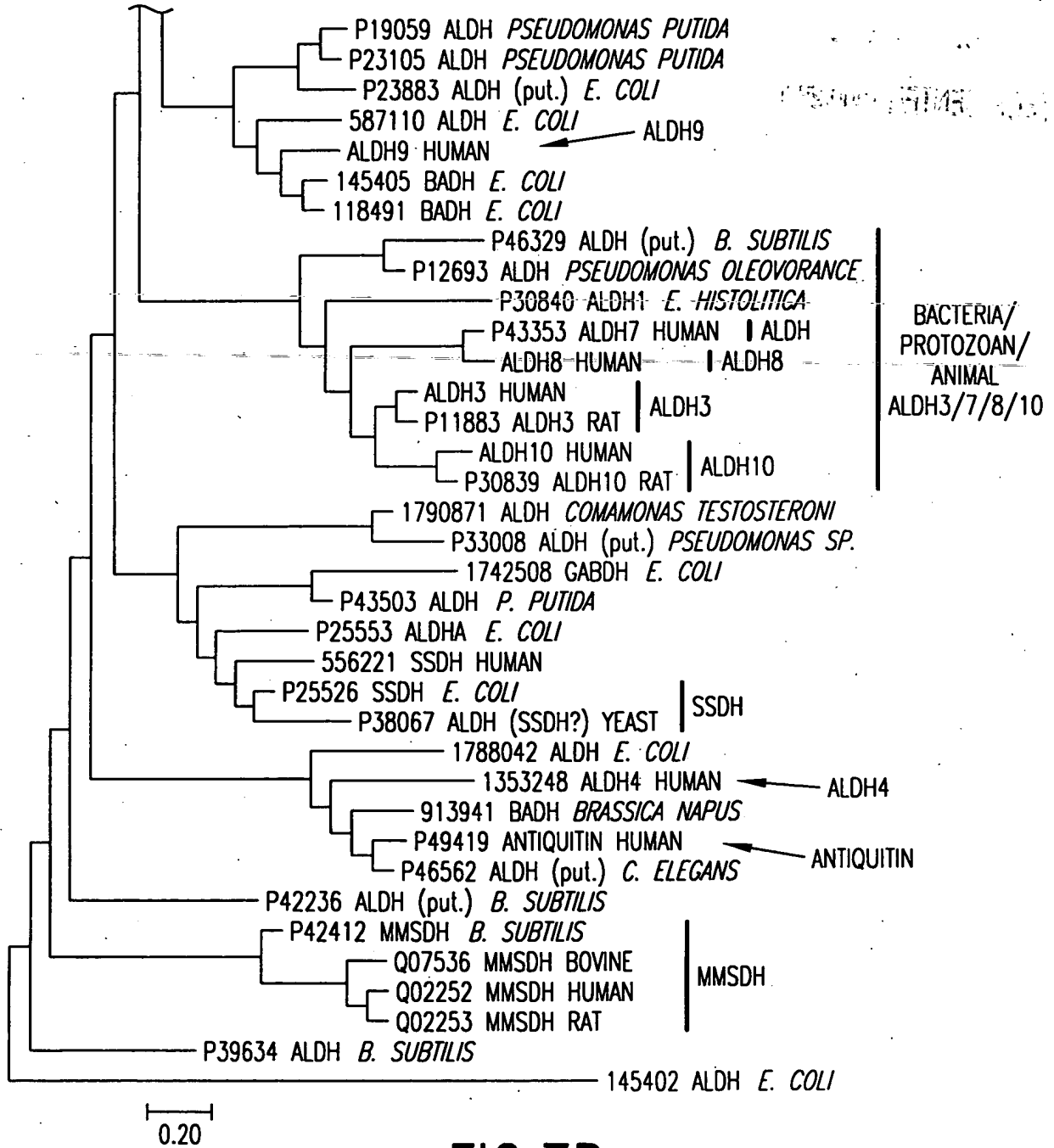
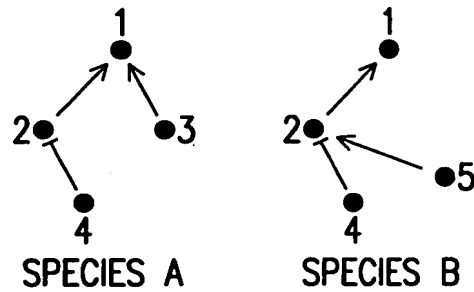


FIG.7B



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← INDUCE  
← ACTIVATE  
⊥ INHIBIT

FIG.9A

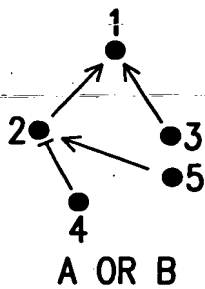


FIG.9B

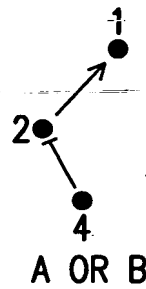


FIG.9C

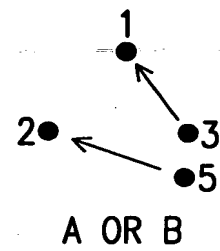


FIG.9D

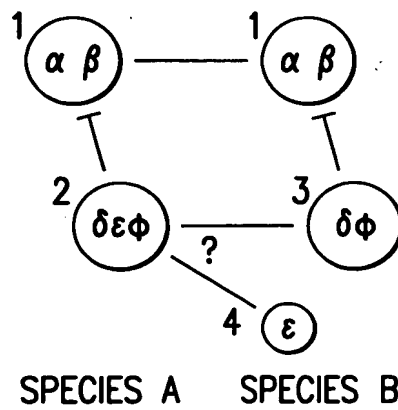


FIG.10

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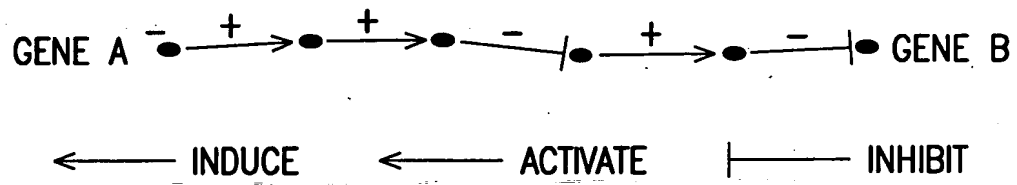


FIG.11A

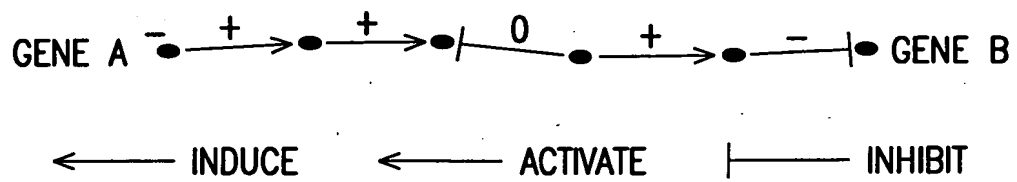


FIG.11B

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FLOW CHART SCHEME OF GENE DISCOVERY ANALYSIS  
INVOLVING MOTIF/DOMAIN ANALYSIS.

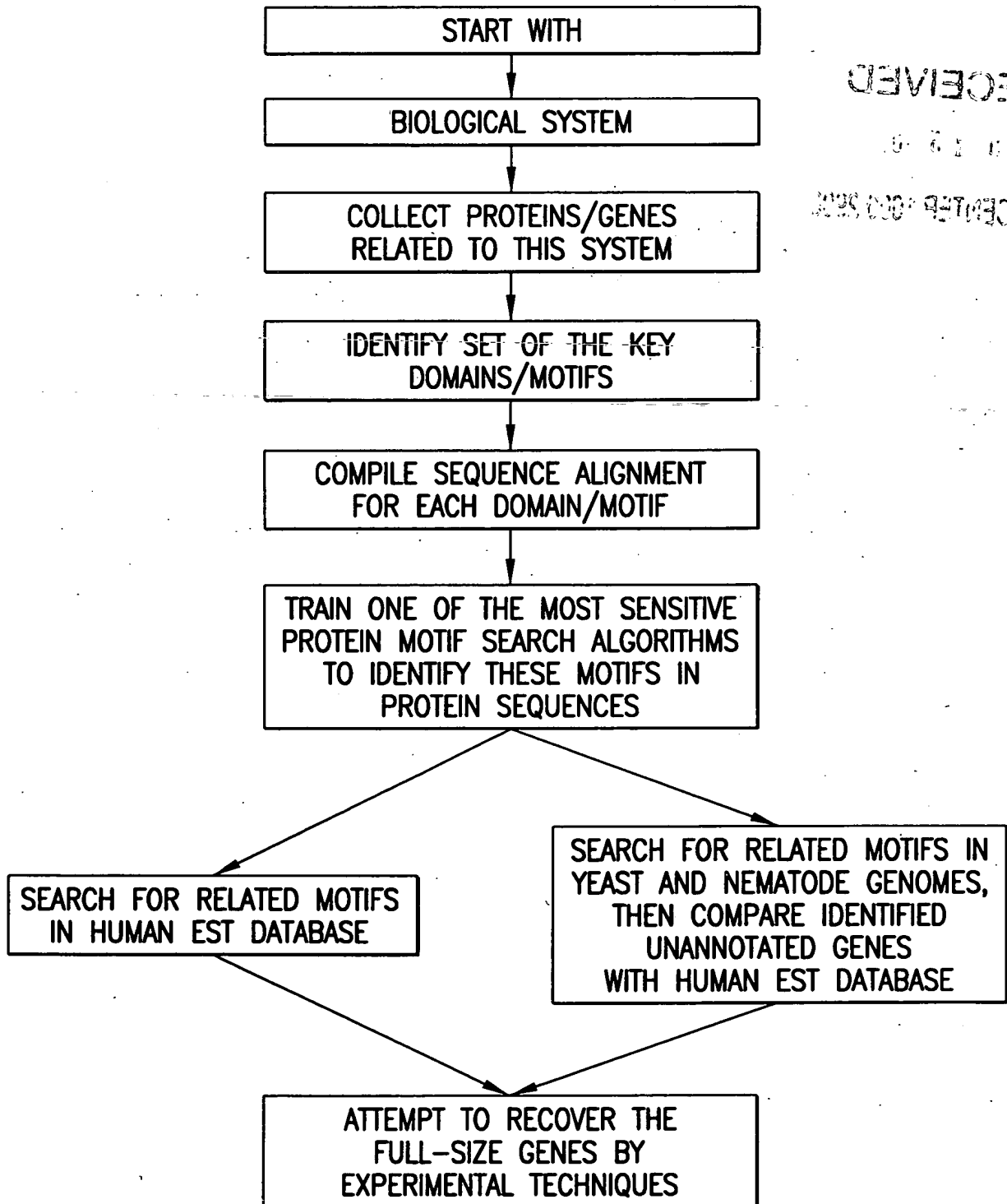
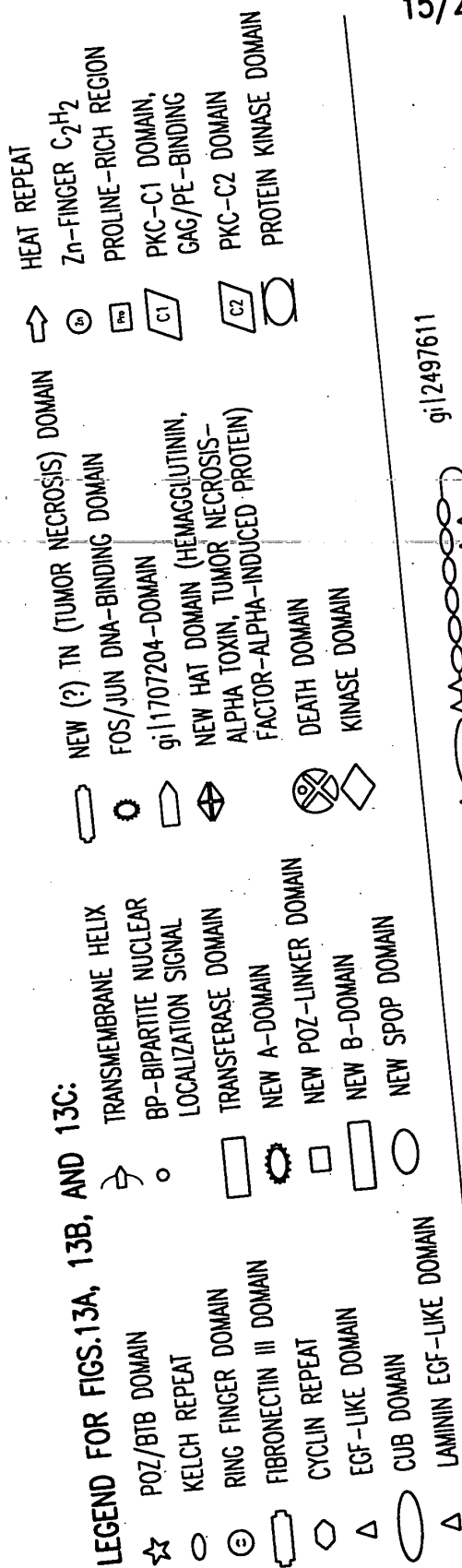


FIG.12



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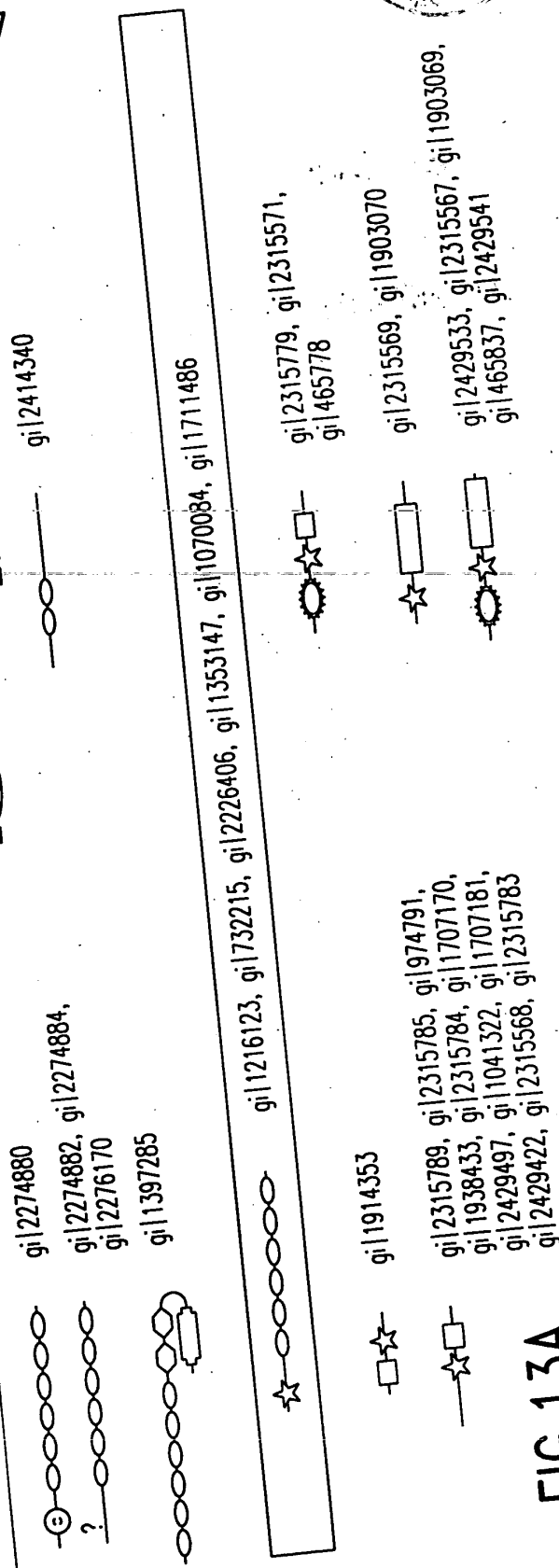


FIG. 13A

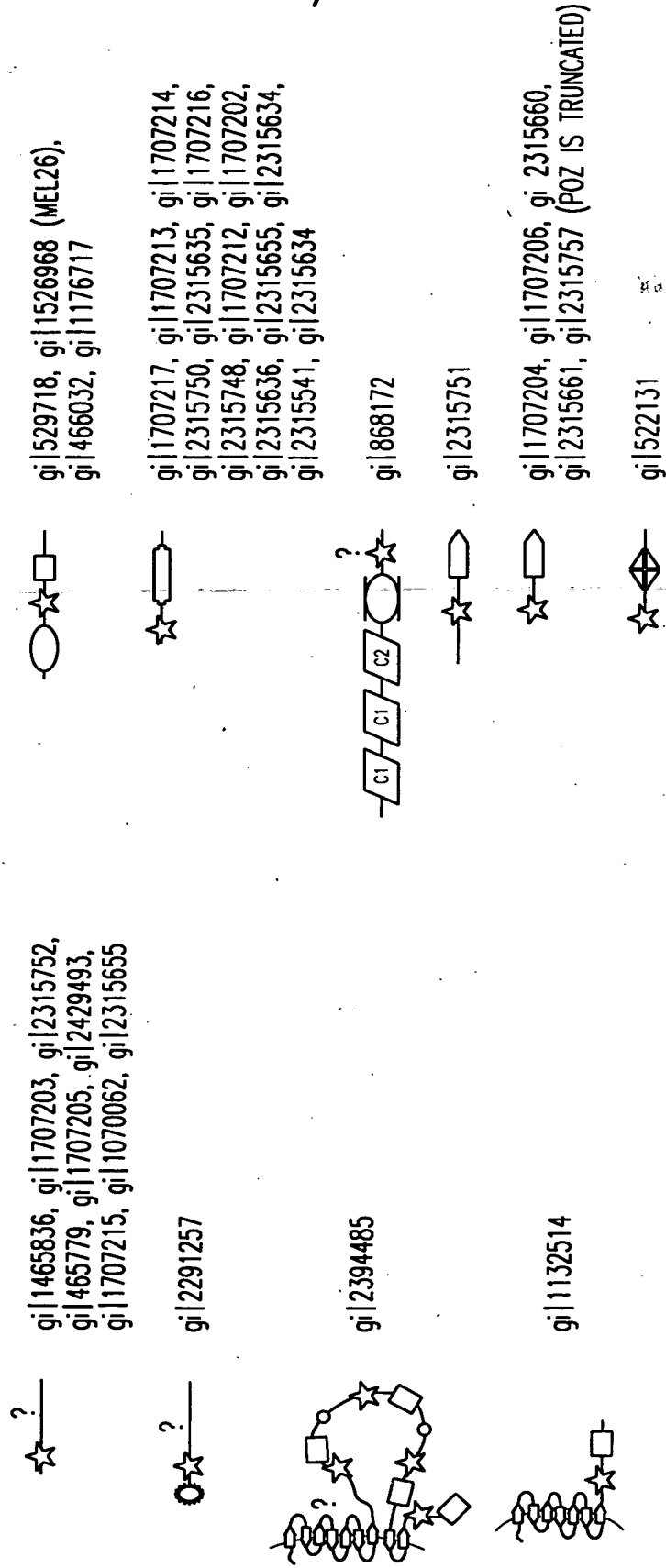
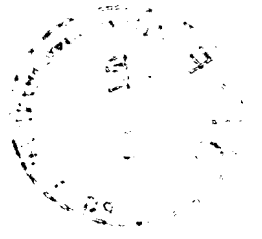


FIG.13B





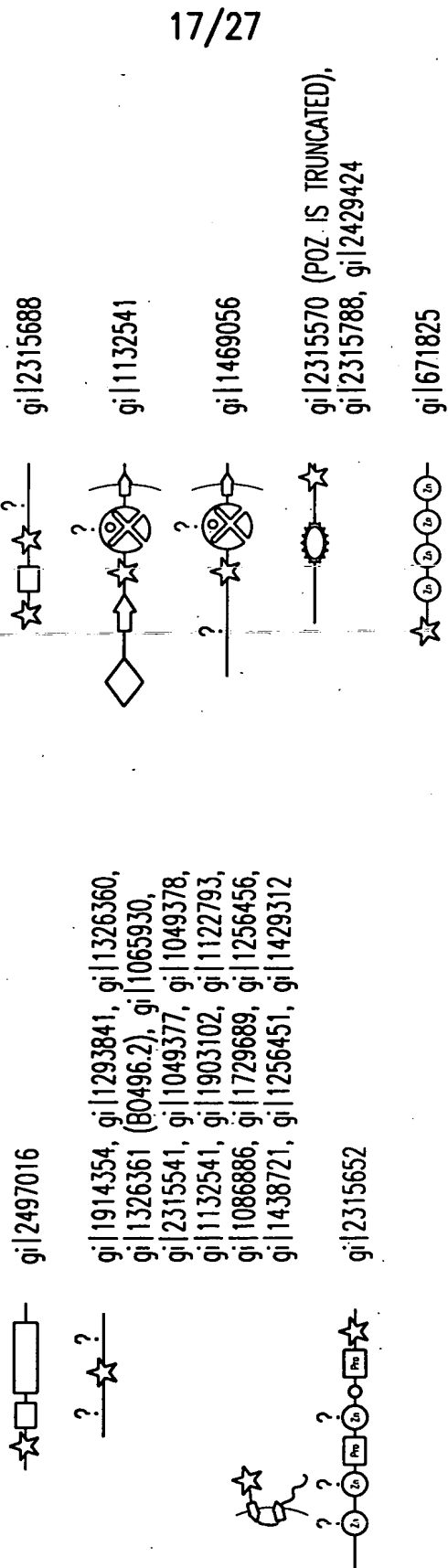
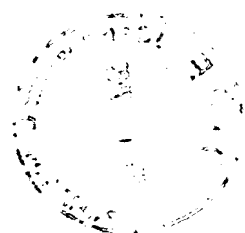


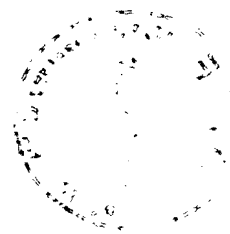
FIG.13C



>gi|2210766|gb|AA481214|AA481214 aa34e02.r1 NCI CGAP\_GCB1 Homo sapiens cDNA clone  
 IMAGE:815162 5' similar to WP:W07A12.4 CE03795 :, mRNA sequence [Homo sapiens]  
 CATGGCTTCTGGACACCAACCCTGCCATCCGGGAGCAGACGGTCAAGTCCATGCTGCTCTGGCCCCCAA  
 AGCTGAACGAGGCCAACCTCAATGTGGAGCTGATGAAGCACCTTGCACGGCTACAGGCCAAGGATGAACA  
 GGGCCCCATCCGCTGCAACACCACAGTCTGCCTGGGCAAAATCGGCTCCTACCTCAGTGCTAGCACCCAGA  
 CACAGGGTCTTACCTCTGCCCTCAGCCGAGCCACTAGGGACCCGTTTGCACCCGTCCCGGGTTGCGGGTG  
 TCCTGGGCTTTGCTGCCACCCACAACCTCTACTCAATGAACGACTGTGCCCCAGAAGATCCTGCCTGTGCT  
 CTGCGGTCTCACTGTAGATCCTGAGAAATCCGTGCGAGACCAGGCCCTTCAAGGCCA

>gi|1349211|gb|W51957|W51957 zc45f01.r1 Soares\_senescent\_fibroblasts\_NbHSF Homo  
 sapiens cDNA clone IMAGE:325273 5', mRNA sequence [Homo sapiens]  
 CCTTCGAGTTCGGCAATGCTGGGGCCGTTGTCTCACGCCCTCTTCAAGGTGGGCAAGTTCTTGAGCGC  
 TGAGGAGTATCAGCAGAAGATCATCCCTGTGGTGGTCAAGATGTTCTCATCCACTGACCGGGCCATGCGC  
 ATCCGNCTCCTGCAGCAGATGGAGCAGTTTCATCCAGTACCTTGACGAGCCAACAGTCAACACCCAGATCT  
 TCCCCACGTCGTACATGGCTTCTTGGACACCAACCTGCCATCCGGGAGCAGACGGTCAAGTCCATGCT  
 GCTCTGGCCCCAAAGCTGAACGAGGCCAACCTCAATGTGGAGCTGATGAAGCACTTTGCACGGCTACAG  
 GCCAAGGATGAACAGGGCCCCATCCGCTGCAACACCACAGTCTGCCTGGGCAAAATCGGCTCCTACCTCA  
 GTGCTAGCACACAGACAGGGTCTTACCTCTG

FIG.14A



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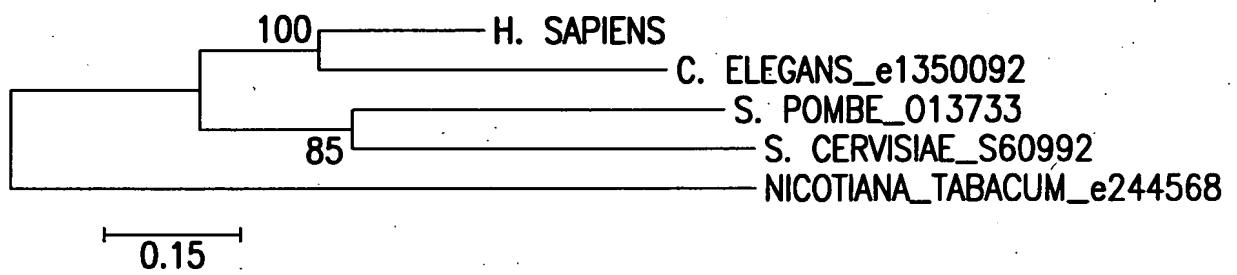


FIG. 14B



BASE COUNT 405 a 545 c 493 g 278 t 6 others

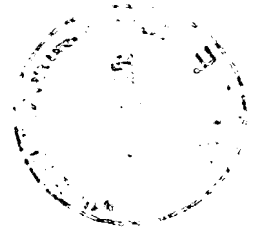
ORIGIN

```

1  cagccgaagc amgcaaaaat tcttccagga gctgagcaag agcctggacg cattccctga
61 ggayttctgt cggcacaagg tgctgcccc a gctgctgacc gccttcgagt tcggcaatgc
121 tggggccggt gtcctcacgc ccctcttcaa ggtgggcaag ttcctgagcg ctgaggagta
181 tcagcagaag atcatccctg tgggtgtcaa gatgttctca tccactgacc gggccatgcg
241 catccgcctc ctgcagcaga tggagcagtt catccagtac cttgacgagc caacagtcaa
301 caccagatc ttccccacg tegtacatgg cttcctggac accaaccctg ccatccggga
361 gcagacggtc aagtccatgc tgctcctggc cccaaagctg aacgaggcca acctcaatgt
421 ggagctgatg aagcactttg cacggctaca ggccaaggat gaacagggcc ccatccgctg
481 caacaccaca gtctgcctgg gcaaaatcgg ctctacctc agtgctagca ccagacacag
541 ggtccttacc tctgccttca gccgagccac tagggaaeeeg tttgcaaccgt cccgggttgc
601 ggggtgtcctg ggctttgctg ccaccacaaa cctctactca atgaacgact gtgcccagaa
661 gatcctgcet gtgetctgcg gtctcactgt agatcctgag aaatccgtgc gagaccaggc
721 cttcaaggcm wttcggagct tcctgtccaa attggagtct gtgtcggagg acccgaccca
781 gctggaggaa gtggagaagg atgtccatgc agcctccagc cctggcatgg gaggagccgc
841 agctagctgg gcaggctggg cgtgaccggg gtctcctcac tcacctcaa gctgatccgt
901 tcgcacccaa ccactgcccc aacagaaacc aacattcccc aaagaccac gcctgaagga
961 gttcctgccc cagccccac ccctgttctt gccacccta caacctcagg ccactgggag
1021 acgcaggagg aggacaagga cacagcagag gacagcagca ctgctgacag atgggacgac
1081 gaagactggg gcagcctgga gcaggaggcc gagtctgtgc tggcccagca ggacgactgg
1141 agcaccgggg gccaaagtga ccgtgctagt caggtcagca actccgacca caaatcctcc
1201 aaatccccag agtccgactg gagcagctgg gaarctgagg gctcctggga acagggctgg
1261 caggagccaa gctcccagga gccacctyct gacggtacac ggctggccag cgagtataac
1321 tggggtggcc cagagtccag cgacaagggc gaccccttcg ctacctgtc tgcacgtccc
1381 agcaccagc cgaggccaga ctcttggggt gaggacaact gggagggcct cgagactgac
1441 agtcgacagg tcaaggctga gctggcccgg aagaagcgcg aggagcggcg gcgggagatg
1501 gaggccaaac gcgccgagag gaaggtgcc aaggcccat gaagctggga gcccggaagc
1561 tggactgaac cgtggcgggt gcccttccc gctgcggaga gcccggccca cagatgtatt
1621 tattgtacaa accatgtgag cccggccgcc cagccaggcc atctcacgtg tacataatca
1681 gagccacaat aaattctatt tcacaaaaaa aaaaaaaaaa aaaaaaa

```

FIG. 14C



5 10 15 20 25 30  
1 SRSXQKFFQELSKSLDAFPEDFCRHKVLPQ  
31 LLTAFEFGNAGAVVLTPLFKVGKFLSAEEY  
61 QQKIIPVVVKMFSS.TDRAMRIRLLQQMEQF  
91 IQYLDEPTVNTQIFPHVVHGFLDTNPAIRE  
121 QTVKSMLLLAPKLN EANLNVELMKHFARLQ  
151 AKDEQGP I RCNTTVCLGKIGSYLSASTRHR  
181 VLTSAFSRATRD PFAPS RVAGVLGFAATHN  
211 LYSMNDC AQKILPVLCGLTVDPEKSVRDQA  
241 FKAXRSFLSKLESVSEDP TQLEEEVEKDVHA  
271 ASSPGMGGAASWAGWA

FIG.14D

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RECEIVED

JUN 19 1997

>sp|P15533|RPT1\_MOUSE DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR  
(J03776) rpt-1r [Mus musculus] Length = 353

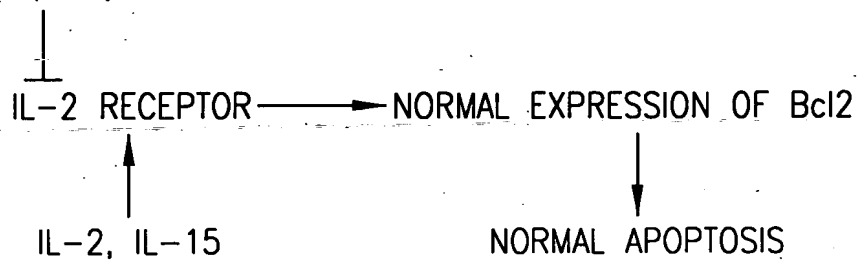
Score = 92.0 bits (237), Expect = 6e-20

Query 194	VMELLEEDLTCPICCSLFDDPRVLPCSHNFCKKCLEGILEGSRNSMWRPAPFKCPTCRK	373
	V+E+++E++TCPIC L +P C+H+FC+ C+ E S RN+ CP CR	
Sbjct 5	VLEMIKEEVTCPICLELLKEPVSADCNHSFCRACITLNYE-SNRNT---DGKGNCPCVCRV	60
Query 374	ETSATGINSLQVNYSLKGIVEKYNKIKISP----KMPVCKGHMGQPLNIFCLTDMQLICG	541
	+L+ N + IVE+ K P K+ +C H G+ L +FC DM +IC	
Sbjct 61	PYP---FGNLRPNLHVANIVERLKGFKSIPEEEQVNICAH-GEKLRLFCRKDMVICW	116
Query 542	ICATRGEHTKHVFCSIEDAYAQERDAFESLFQSF-----ETWRRGDALSRLDTMETSK	700
	+C EH H IE+ + + + + + W+ L R+D	
Sbjct 117	LCERSQEHGRGHQTALIEEVDQEYKEKLQGALWKLMMKAKICDEWQDDLQLQRVDW-----	171
Query 701	RKSLQLMTKDSKVKKEFFEKLQHTLDQKKNEILSDFETMKLAVMQAYDPEINKL	862
	+Q+ + + V+ F+ L+ LD K+NE L + K VM+ + N+L	
Sbjct 172	ENQIQI---NVENVQRQFKGLRDLLDSKENEELQKLKKEKKEVMEKLEESENEL	222

FIG.15

ACTIVATED CD4<sup>+</sup> T-CELLS

Rpt1 (REPRESSES EXPRESSION OF IL-2 RECEPTOR)



## WHEN rpt1 IS KNOCKED OUT:

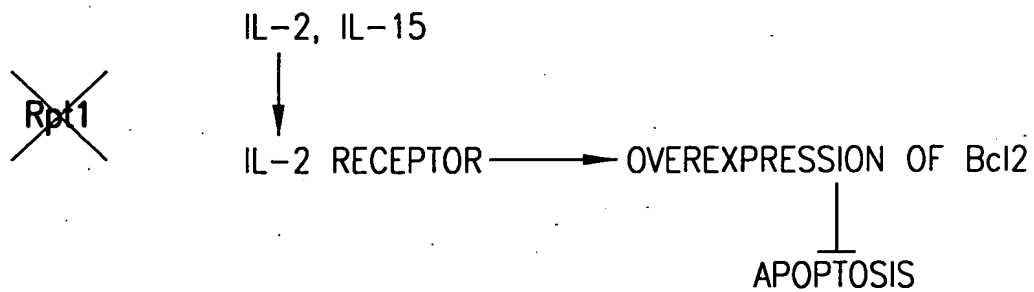


FIG. 16



Query= gi |2137498|Mad3m  
(205 letters)

gb|AA278224|AA2278224 zs77e05.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:703520 5'  
similar to TR:G1184157 G1184157 MAX-INTERACTING  
TRANSCRIPTIONAL REPRESSOR. ;  
Length = 430

Score = 209 bits (526), Expect = 1e-53  
Identities = 104/124 (83%), Positives = 116/124 (92%), Gaps = 1/124 (0%)  
Frame = +2

Query: 1 MEPVASNIQVLLQAAEFLERREREAEHGYASLCPHHSPGTVCRRRKPPLQAPGALNSGRS 60  
MEP+ASNIQVLLQAAEFLERREREAEHGYASLCPH SPG + RR+K P QAPGA +SGRS  
Sbjct: 56 MEPLASNIQVLLQAAEFLERREREAEHGYASLCPHRSPGPIHRRKKRPPQAPGAQDSGRS 235

Query: 61 VHNELEKRRRAQLKRCLEQLRQQMPLGVDCTRYTTL SLL -RARVHIQKLEEQEQQARRLK 119  
VHNELEKRRRAQLKRCLE+L+QQMPLG DC RYTTL SLL RAR+HIQKLE+QE+AR+LK  
Sbjct: 236 VHNELEKRRRAQLKRCLERLKQQMPLGGDCARYTTL SLLRRARMHIQKLEDQEQRARQLK 415

Query: 120 EKLRS 124  
E+LR+  
Sbjct: 416 ERLRT 430

dbj|C02407|C02407 HUMGS0012279, Human Gene Signature, 3'-directed cDNA sequence.  
Length = 348

Score = 97.5 bits (239), Expect = 6e-20  
Identities = 51/63 (80%), Positives = 56/63 (87%)  
Frame = +3

Query: 125 KQQSLQQLEQLQGLPGARERERLRADSLDSSGLSSERSDSDQEDLEVDVENLVFGTETE 184  
KQQSLQ+ QL+GL GA ERERLRADSLDSSGLSSERSDSDQE+LEVDVE+LVFG E E  
Sbjct: 45 KQQSLQRXWMQLRGLAGAAERERLRADSLDSSGLSSERSDSDQEELEVDVESLVFGGEAE 224

Query: 185 LLQ 187  
LL+  
Sbjct: 225 LLR 233

FIG.17A



BASE COUNT 130 a 234 c 258 g 106 t 5 others  
 ORIGIN

```

1  cagccgcttg ctccggccgg caccctaggc cgcagtccgc caggctgtcg ccgacatgga
61 acccttggcc agcaacatcc aggtcctgct gcaggcggcc gagttcctgg agcgccgtga
121 gagagaggcc gageatgggt atgegteect gtgeeegeat egeagtecag gccccatcca
181 caggaggaag aagcgacccc ccagggctcc tggcgcgag gacagcgggc ggtcagtgca
241 caatgaactg gagaagcgca ggagggccca gttgaagcgg tgcctggagc ggctgaagca
301 gcagatgccc ctgggcggcg actgtgcccg gtacaccacg ctgagcctgc tgcgccgtgc
361 caggatgcac atccagaagc tggaggatca ggagcagcgg gcccgacagc tcaaggagag
421 gctgcgaca aagcagcaga gcctgcagcg gcantggatg cagctccggg ggctggcagg
481 ngcggccgag cgggagcgnc tgcgggcgga cagtctggac tcctcaggcc tctcctctga
541 gcgctcagac tcagaccaag aggagctgga ggtggatgtg gagagcctgg tgtttggggg
601 tgaggccgag ctgctgcggg gcttcgtcgc cggccaggag cacagctact cgcacgtcgg
661 cggcgccctg ctatgatgtt cctcaccan ggcgggcctc tgccctctta ctcgttgccc
721 aagcccactt tnc

```

FIG.17B

>Mac3b (Putative)

MEPLASNIQVLLQAAEFLERREREAEHGYASLCPHRSPGIHRRKKRPPQAPGAQDSGRSVHNELEKRRRAQLK  
RCLERLKQQMPLGGDCARYTTLSSLRRARMHIKLEDEQERARQLKERLRTKQSLQRXWMQLRGLAGAAERER  
LRADSLDSSGLSSERSDSDOEELEVDVESLVFGGEAELLRGFVAGOEHSYSHVGGAWL

## FIG.17C

gi | 2506888 | MADe  
gi | 729978 | MADh  
gi | 2792362 | Mad4h  
gi | 217199 | Mad4m  
gi | 2137199 | Mad3m  
Mad3h Putative

MATAVGHNIIQLLEAADYLERREAEHGYASMLPYS-KDADAFKRRNKPKKNST--SSRSTHMEMEKNNRAHLRLCLEKLGVLPGPSSRHTTLLSLL  
MAAAYRMNIQMLLEAADYLERREAEHGYASMLPYNNKORDALKRRNKKNNNS--SSRSTHMEMEKNNRAHLRLCLEKLGVLPGPSSRHTTLLSLL  
---MELNSLLILLEAAEYLERRDREAEHGYASVLPFDGDFAREKTKAAGLVKAP--NNRSSHNELEKHRRAKLRLYLEQLKQLVPLGPDSTRHTTLLSLL  
---MELNSLLLLLEAAEYLERRDREAEHGYASMLPFDGDFARKTKTAGLVKGP--NNRSSHNELEKHRRAKLRLYLEQLKQLGPLGPDSTRHTTLLSLL  
-MEPVASNIQVLLQAAEFLERREREAEHGYASLCPHSPGTVCRRKPPLOAPGALNSGRSVHNELEKRRRAQLKRCLEQLRQQMPLGVDCTRYTTLSSL  
-MEPLASNIQVLLQAAEFLERREREAEHGYASLCPHRSPGIHRRKKRPPQAPGAQDSGRSVHNELEKRRRAQLKRCLERLKQQMPLGGDCARYTTLSSL

gi | 2506888 | MADe  
gi | 729978 | MADh  
gi | 2792362 | Mad4h  
gi | 2137499 | Mad4m  
gi | 2137498 | Mad3m  
Mad3h Putative

TKAKLHTIKKLEDCORKAVHQIDQLQREQRHLKRRLEKLGAEIR-----MDSVG-SWSSERSDSREELDVIDVDVDVEGTDYLPGDLGWSS-  
TKAKLHTIKKLEDCORKAVHQIDQLQREQRHLKRRLEKLGIERIR-----MDSIG-STVSSERSDSRE-----EIDVDVESTDYLTGDLDMSSSS  
KRAKVHTIKKLEEQRRALSTKEQLQOEHRFLKRRLEQLSVQSVR-----VRTDSTG-SAVSTD--DSEQE-----VDIEGMEFGPGELDSVGS-  
K-AKMHITKLEEQRRALSTKEQLQREHRFLKRRLEQLSVQSVR-----VRTDSTG-SAVSTD--DSEQE-----VDIEGMEFGPGELDSAGS-  
R-ARVHTIKLEEQEQARRLKEKLRKQSLQOQLQGLPGAREPRRLPADSLDSSGLSSERSDSDOE-----DLSVDVENLVFG-TETELLQSF  
RRARMHIKLEDEQERARQLKERLRTKQSLQRXWMQLRGLAGAAERERLRADSLDSSGLSSERSDSDOE-----ELEVDVESLVFG-GEAELLRGF

gi | 2506888 | MADe  
gi | 729978 | MADh  
gi | 2792362 | Mad4h  
gi | 2137499 | Mad4m  
gi | 2137498 | Mad3m  
Mad3h Putative

VSDSDESGSMQSLG-SDEGYSSATVKRAKLQQGHKAGLGL  
VSDSDESGSMQSLG-SDEGYSSSTIKRIKLQOSHAKLGL  
SSDADHYSLQSGTGGDSGFGPHCRRLGRPALS-----  
SSDADHYSLQSSGCSDSYVGHPCRRPGCPGLS-----  
SAGREHSYSHSTCAWL-----  
VAGQEHSYSHVGGAWL-----

## FIG.17D

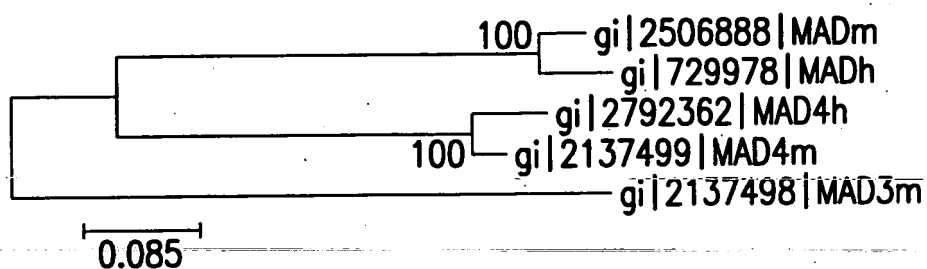


FIG.18A

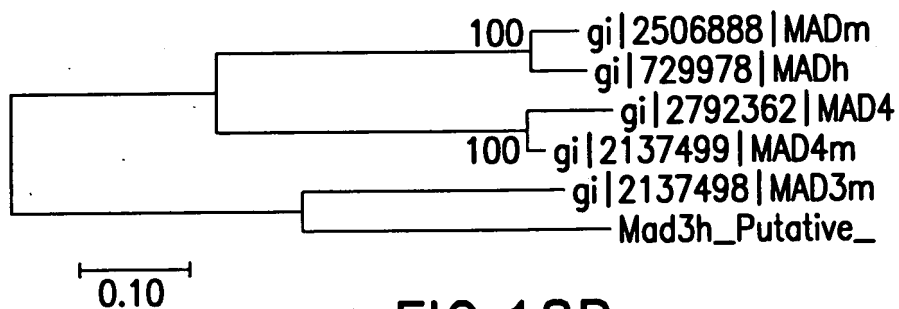


FIG.18B